



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/786675A

Source: OIPE

Date Processed by STIC: 09/19/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

09/786 675A

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER:

09/728497A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
"bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s). Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
(OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
(NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 9 Use of n's or Xaa's
(NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213>
Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
"bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

AMC/MH - Biotechnology Systems Branch - 08/21/2001

The type of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

OIPE

RAW SEQUENCE LISTING

DATE: 09/19/2001

PATENT APPLICATION: US/09/786,675A

TIME: 10:20:21

Input Set : A:\BB-1240 Seq List - Corrections.txt

Output Set: N:\CRF3\09192001\I786675A.raw

Does Not Comply
Corrected Diskette Needed

```

3 <110> APPLICANT: Cahoon, Rebecca E
4     Miao, Gou-Hau
5     Powell, Wayne
7 <120> TITLE OF INVENTION: Plant Farnesyltransferases
9 <130> FILE REFERENCE: BB-1240
11 <140> CURRENT APPLICATION NUMBER: US/09/786,675A
C--> 12 <141> CURRENT FILING DATE: 2001-08-29
14 <150> PRIOR APPLICATION NUMBER: 60/099,521
15 <151> PRIOR FILING DATE: 1998-09-08
17 <160> NUMBER OF SEQ ID NOS: 23
19 <170> SOFTWARE: Microsoft Word Version 7.0A
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 1426
23 <212> TYPE: DNA
24 <213> ORGANISM: Zea mays
26 <400> SEQUENCE: 1
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28 cagctggact catcgcccat ggagcacact aagtcaggcc ccagcagttg gccagaactg 120
29 gccgacgtgg tgccgggtgcc gcaggacgat gggcctagcc ctgtggtgtc catcgctat 180
30 cgagatgact ttcgtagagt catggattac ttccgcgccc tctacctcac cggtgagcga 240
31 agccctcgcg ctctccgcct caccgcccag gccatcgagc tcaaccccg caactacact 300
32 gtctggcatt tccggcgctt tattctggag tctactagatt ttgatttact agaggagatg 360
33 aaatttgctg aaaaaattgc tgaatgcaat ccaaaaaatt accaaatctg gcaccataag 420
34 agatggcttg ctgagaaatt aggacctggg attgcaaaca aagagcatga attcacaatg 480
35 aagatacttg ctattgatgc aaaaaattat catgcttggg ctcataggca gtgggttctt 540
36 caagcgcttg ggggatggga gactgaatta gaatactgtg accacttact taaggagac 600
37 gtcttcaata attcagcttg gaatcagaga tactttgtta taacaagatc accatttctt 660
38 ggtggccttg cggcaatgcg tgattcagaa gtagactaca caattgaagc tattctagca 720
39 aacgctcaga atgaaagccc ctggagggtac ctcaagggtc tatacaaggg tgagaataac 780
40 ctgctagtag aggacgagcg catctctgct gtttgtttca aggtcctgaa gaatgattgg 840
41 acttggtgat ttgctttgag tttgctgctc gatcttctct gcaactggtt gcagccttca 900
42 gatgaactta ggtccactct tgaacaata aggagctccc atcctgaaac cgcggatgat 960
43 gatcctgcag ccgctgtttg ctgtatcctg cagaaatgtg atcccctgcg ggtaaattat 1020
44 tggctcttgg tcaaggacac tctttctcag atctcatgac ttcacatggg ttcacccctt 1080
45 gtccgcgctg gtccgggctc tgtgagatag acatgtttta gatagtttca ttggacaccc 1140
46 aaacagagcg gacagagtgt atggctgcta ccttctccgt gactgaaagc agtgcttgta 1200
47 acgattttgt ttagtaaaat ttgtgagtgt tactgtcca aacaacacct tatgcaacca 1260
48 tatttgataa ttccacatgt aagcttgaat ccaggtgtgt ttgttaatgt attacaattg 1320
49 ccatgggagc ctaaatgaga ccataatca cttccactag agtcggaaga ccgtgtcgag 1380
50 cagttcactc atatggtcac ttaaagcaaa aaaaaaaaaa aaaaaa 1426
52 <210> SEQ ID NO: 2
53 <211> LENGTH: 326
54 <212> TYPE: PRT
55 <213> ORGANISM: Zea mays
57 <400> SEQUENCE: 2
58 Met Glu His Thr Lys Ser Gly Pro Ser Ser Trp Pro Glu Leu Ala Asp
59 1 5 10 15

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61 Val Val Pro Val Pro Gln Asp Asp Gly Pro Ser Pro Val Val Ser Ile
62          20          25          30
64 Ala Tyr Arg Asp Asp Phe Arg Glu Val Met Asp Tyr Phe Arg Ala Leu
65          35          40          45
67 Tyr Leu Thr Gly Glu Arg Ser Pro Arg Ala Leu Arg Leu Thr Ala Glu
68          50          55          60
70 Ala Ile Glu Leu Asn Pro Gly Asn Tyr Thr Val Trp His Phe Arg Arg
71 65          70          75          80
73 Leu Ile Leu Glu Ser Leu Asp Phe Asp Leu Leu Glu Glu Met Lys Phe
74          85          90          95
76 Val Glu Lys Ile Ala Glu Cys Asn Pro Lys Asn Tyr Gln Ile Trp His
77          100          105          110
79 His Lys Arg Trp Leu Ala Glu Lys Leu Gly Pro Gly Ile Ala Asn Lys
80          115          120          125
82 Glu His Glu Phe Thr Met Lys Ile Leu Ala Ile Asp Ala Lys Asn Tyr
83          130          135          140
85 His Ala Trp Ser His Arg Gln Trp Val Leu Gln Ala Leu Gly Gly Trp
86 145          150          155          160
88 Glu Thr Glu Leu Glu Tyr Cys Asp His Leu Leu Lys Glu Asp Val Phe
89          165          170          175
91 Asn Asn Ser Ala Trp Asn Gln Arg Tyr Phe Val Ile Thr Arg Ser Pro
92          180          185          190
94 Phe Leu Gly Gly Leu Ala Ala Met Arg Asp Ser Glu Val Asp Tyr Thr
95          195          200          205
97 Ile Glu Ala Ile Leu Ala Asn Ala Gln Asn Glu Ser Pro Trp Arg Tyr
98          210          215          220
100 Leu Lys Gly Leu Tyr Lys Gly Glu Asn Asn Leu Leu Val Glu Asp Glu
101 225          230          235          240
103 Arg Ile Ser Ala Val Cys Phe Lys Val Leu Lys Asn Asp Trp Thr Cys
104          245          250          255
106 Val Phe Ala Leu Ser Leu Leu Leu Asp Leu Leu Cys Thr Gly Leu Gln
107          260          265          270
109 Pro Ser Asp Glu Leu Arg Ser Thr Leu Glu Thr Ile Arg Ser Ser His
110          275          280          285
112 Pro Glu Thr Ala Asp Asp Asp Pro Ala Ala Ala Val Cys Cys Ile Leu
113          290          295          300
115 Gln Lys Cys Asp Pro Leu Arg Val Asn Tyr Trp Ser Trp Phe Lys Asp
116 305          310          315          320
118 Thr Leu Ser Gln Ile Ser
119          325
121 <210> SEQ ID NO: 3
122 <211> LENGTH: 1218
123 <212> TYPE: DNA
124 <213> ORGANISM: Oryza sativa
126 <400> SEQUENCE: 3
127 gcacgaggtt ctaacgccgc cgccgccgcc gccgtctccg cagaatctga tcgatggcgc 60
128 cgctcgtcgac gtcgtcggag ggtgcctccg acgagtgggt gccacccagc cggcgggccg 120
129 agctggcgga cgtgggtcccc gtgacgcagg acgacgggcc ccaccccggt gtggccatcg 180
130 cctaccggga cgagttccgc gaggtcatgg actacttccg cgccctctac ttcgccggcg 240

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Input Set : A:\BB-1240 Seq List - Corrections.txt

Output Set: N:\CRF3\09192001\I786675A.raw

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131 agcgcagcgt ccgcgccttc cacctcaccg ccgagggtcat cgaccttaat cccggcaact 300
132 acacgggtgtg gcatttttagg cgtcttggtc tagaggcact ggatgctgat ctgcgtgagg 360
133 aaatggattt tgtggaccga attgctgaat gtaacccaaa aaattatcaa atctggcatc 420
134 acaagagatg gcttgccggag aaattaggac cagatattgc aaataaagag cacgaattta 480
135 caaggaagat actttctatg gatgctaaaa attaccatgc ttggtctcat aggcagtggg 540
136 ttcttcaagc actgggtgga tgggagactg aactacagta ttgcaaccag ctgcttgagg 600
137 aagacgtctt caataattca gcttggaatc agagatacct tgtaataaca agttcaccac 660
138 ttcttgaggg ccttgcagca atgcgtgact cggaagtgga ttacacagtt ggggctattc 720
139 tggctaacc ctcagaatgaa agcccctgga gatacctcaa aggcctgtac aagggtgaaa 780
140 ataacttgct gatggctgat gagcgcact ctgatgtttg tctcaaggtc ctgaaacatg 840
141 attcgacctg cgtatttgct ttgagcttgc tgctcgatct tcttcaaatt ggtttacaac 900
142 cttcagatga actcaaagga actatcgaag caataaagaa ctctgatcct gaagcagatg 960
143 aagcagtaga tgctgatctt gcgactgcaa tctgtcfaat attgcagaga tgtgatcccc 1020
144 tgcggataaa ttactgggtcc tggtagagga ccactatttc ttctcaaacc tgaagcatgc 1080
145 agtggcctcc atgaggctcat aatggagata tcttctatct tcgtgtgatt ctgggcgttg 1140
146 aggtgcctag ctacatttgt tatgaacttt ccttgggcat aactgatcac tgatattact 1200
147 ccaatattgt gttctaaa 1218
149 <210> SEQ ID NO: 4
150 <211> LENGTH: 339
151 <212> TYPE: PRT
152 <213> ORGANISM: Oryza sativa
154 <400> SEQUENCE: 4
155 Met Ala Pro Ser Ser Thr Ser Ser Glu Gly Ala Ser Asp Glu Trp Leu
156 1 5 10 15
158 Pro Pro Ser Arg Arg Pro Glu Leu Ala Asp Val Val Pro Val Thr Gln
159 20 25 30
161 Asp Asp Gly Pro His Pro Val Val Ala Ile Ala Tyr Arg Asp Glu Phe
162 35 40 45
164 Arg Glu Val Met Asp Tyr Phe Arg Ala Leu Tyr Phe Ala Gly Glu Arg
165 50 55 60
167 Ser Val Arg Ala Leu His Leu Thr Ala Glu Val Ile Asp Leu Asn Pro
168 65 70 75 80
170 Gly Asn Tyr Thr Val Trp His Phe Arg Arg Leu Val Leu Glu Ala Leu
171 85 90 95
173 Asp Ala Asp Leu Arg Glu Glu Met Asp Phe Val Asp Arg Ile Ala Glu
174 100 105 110
176 Cys Asn Pro Lys Asn Tyr Gln Ile Trp His His Lys Arg Trp Leu Ala
177 115 120 125
179 Glu Lys Leu Gly Pro Asp Ile Ala Asn Lys Glu His Glu Phe Thr Arg
180 130 135 140
182 Lys Ile Leu Ser Met Asp Ala Lys Asn Tyr His Ala Trp Ser His Arg
183 145 150 155 160
185 Gln Trp Val Leu Gln Ala Leu Gly Gly Trp Glu Thr Glu Leu Gln Tyr
186 165 170 175
188 Cys Asn Gln Leu Leu Glu Glu Asp Val Phe Asn Asn Ser Ala Trp Asn
189 180 185 190
191 Gln Arg Tyr Leu Val Ile Thr Ser Ser Pro Leu Leu Gly Gly Leu Ala
192 195 200 205
194 Ala Met Arg Asp Ser Glu Val Asp Tyr Thr Val Gly Ala Ile Leu Ala

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Output Set: N:\CRF3\09192001\I786675A.raw

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195      210      215      220
197 Asn Pro Gln Asn Glu Ser Pro Trp Arg Tyr Leu Lys Gly Leu Tyr Lys
198 225      230      235      240
200 Gly Glu Asn Asn Leu Leu Met Ala Asp Glu Arg Ile Ser Asp Val Cys
201      245      250      255
203 Leu Lys Val Leu Lys His Asp Ser Thr Cys Val Phe Ala Leu Ser Leu
204      260      265      270
206 Leu Leu Asp Leu Leu Gln Ile Gly Leu Gln Pro Ser Asp Glu Leu Lys
207      275      280      285
209 Gly Thr Ile Glu Ala Ile Lys Asn Ser Asp Pro Glu Ala Asp Glu Ala
210      290      295      300
212 Val Asp Ala Asp Leu Ala Thr Ala Ile Cys Ser Ile Leu Gln Arg Cys
213 305      310      315      320
215 Asp Pro Leu Arg Ile Asn Tyr Trp Ser Trp Tyr Arg Thr Thr Ile Ser
216      325      330      335
218 Ser Gln Thr
221 <210> SEQ ID NO: 5
222 <211> LENGTH: 1261
223 <212> TYPE: DNA
224 <213> ORGANISM: Glycine max
226 <400> SEQUENCE: 5
227 gcacgaggat taacgaagga tggaatctgg gtctagcgaa ggagaagagg tgcagcaacg 60
228 cgtgccgttg agggagagag tggagtggtc agatgttact ccggttcctc aaaacgacgg 120
229 ccctaaccct gtcgttcoga tccagtacac tgaagagttt tccgaagtta tggattactt 180
230 tcgcgcgctt tacctcaccg atgaacgctc cctcgcgcgc ctcgctctca cagccgaagc 240
231 cgttcaattc aactccggca actacactgt gtggcatttc cgacggttgt tacttgagtc 300
232 gctaaaagtc gacttgaacg atgaactgga ttttgtggag cgtatggccg ctggaaattc 360
233 taaaaattat catagtgggc atcatagacg atgggttgcc gagaagttag gtccctgaagc 420
234 tagaaacaat gagctcgagt tcaccaaaaa gatactgtcc gttgatgcca aacattatca 480
235 tgcattgtct catagacagt gggctcttca aacactagga ggatgggaag atgaacttaa 540
236 ttattgcaca gaactactta aagaagacat ttttaacaat tctgcttgga atcagagata 600
237 ttttgtcata acaaggtctc ctttcttggg gggcctaaaa gctatgagag agtctgaagt 660
238 gctttacacc attgaagcca ttatagccta cctgaaaaat gaaagctcgt ggagatatct 720
239 acgaggactt tataaagggtg aaactacttc atgggtaaat gatcctcaag tttcttcagt 780
240 atgcttaaaag attttgagaa ctaagagcaa ctacgtgttt gctcttagca ctattttaga 840
241 tcttatatgc tttgtttatc aaccaaataa agacattaga gatgccattg acgccttaaa 900
242 gaccgcagat atggataaac aagatttaga tgatgatgag aaaggggaac aacaaaattt 960
243 aaatatagca cgaatatatt gttctatcct aaaacaagtt gatccaatta gaaccaacta 1020
244 ttggatttgg cgcaagagca gacttcctct atcagcttag taaccaaaagt aattaaaggg 1080
245 caactctgtg ttatgtgtaa cctagtttat tgaaactgga tttttattta ttattatttt 1140
246 ttatgttgtc atgtatctgt ttgtgcaaat ttatcttttt gtcattgccat tactggcatt 1200
247 tgagtgtgta gattgaaagc catgcagaat aagaaattta agtttttttt tccgttgaaa 1260
248 a 1261
250 <210> SEQ ID NO: 6
251 <211> LENGTH: 346
252 <212> TYPE: PRT
253 <213> ORGANISM: Glycine max is not an organism
255 <400> SEQUENCE: 6
256 Met Glu Ser Gly Ser Ser Glu Gly Glu Glu Val Gln Gln Arg Val Pro

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Invalid 213 response:
Glycine Max is not an
organism.

Appropriate responses are
"Artificial Sequence", "Unknown"
or the name of some specific
species.

The type of errors shown exist throughout
the Sequence Listing. Please check subsequent
sequences for similar errors.

RAW SEQUENCE LISTING

DATE: 09/19/2001

PATENT APPLICATION: US/09/786,675A

TIME: 10:20:21

Input Set : A:\BB-1240 Seq List - Corrections.txt

Output Set: N:\CRF3\09192001\I786675A.raw

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257   1               5               10               15
259 Leu Arg Glu Arg Val Glu Trp Ser Asp Val Thr Pro Val Pro Gln Asn
260               20               25               30
262 Asp Gly Pro Asn Pro Val Val Pro Ile Gln Tyr Thr Glu Glu Phe Ser
263               35               40               45
265 Glu Val Met Asp Tyr Phe Arg Ala Val Tyr Leu Thr Asp Glu Arg Ser
266               50               55               60
268 Pro Arg Ala Leu Ala Leu Thr Ala Glu Ala Val Gln Phe Asn Ser Gly
269   65               70               75               80
271 Asn Tyr Thr Val Trp His Phe Arg Arg Leu Leu Leu Glu Ser Leu Lys
272               85               90               95
274 Val Asp Leu Asn Asp Glu Leu Asp Phe Val Glu Arg Met Ala Ala Gly
275               100              105              110
277 Asn Ser Lys Asn Tyr Gln Met Trp His His Arg Arg Trp Val Ala Glu
278               115              120              125
280 Lys Leu Gly Pro Glu Ala Arg Asn Asn Glu Leu Glu Phe Thr Lys Lys
281               130              135              140
283 Ile Leu Ser Val Asp Ala Lys His Tyr His Ala Trp Ser His Arg Gln
284 145              150              155              160
286 Trp Ala Leu Gln Thr Leu Gly Gly Trp Glu Asp Glu Leu Asn Tyr Cys
287               165              170              175
289 Thr Glu Leu Leu Lys Glu Asp Ile Phe Asn Asn Ser Ala Trp Asn Gln
290               180              185              190
292 Arg Tyr Phe Val Ile Thr Arg Ser Pro Phe Leu Gly Gly Leu Lys Ala
293               195              200              205
295 Met Arg Glu Ser Glu Val Leu Tyr Thr Ile Glu Ala Ile Ile Ala Tyr
296               210              215              220
298 Pro Glu Asn Glu Ser Ser Trp Arg Tyr Leu Arg Gly Leu Tyr Lys Gly
299 225              230              235              240
301 Glu Thr Thr Ser Trp Val Asn Asp Pro Gln Val Ser Ser Val Cys Leu
302               245              250              255
304 Lys Ile Leu Arg Thr Lys Ser Asn Tyr Val Phe Ala Leu Ser Thr Ile
305               260              265              270
307 Leu Asp Leu Ile Cys Phe Gly Tyr Gln Pro Asn Glu Asp Ile Arg Asp
308               275              280              285
310 Ala Ile Asp Ala Leu Lys Thr Ala Asp Met Asp Lys Gln Asp Leu Asp
311   290              295              300
313 Asp Asp Glu Lys Gly Glu Gln Gln Asn Leu Asn Ile Ala Arg Asn Ile
314 305              310              315              320
316 Cys Ser Ile Leu Lys Gln Val Asp Pro Ile Arg Thr Asn Tyr Trp Ile
317               325              330              335
319 Trp Arg Lys Ser Arg Leu Pro Leu Ser Ala
320               340              345
322 <210> SEQ ID NO: 7
323 <211> LENGTH: 1333
324 <212> TYPE: DNA
325 <213> ORGANISM: Glycine max
327 <400> SEQUENCE: 7
328 gcacgagctt gcgtgtggag tgaagaagat taacgaagga tggaatctgg gtctagcgaa 60

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VERIFICATION SUMMARY

DATE: 09/19/2001

PATENT APPLICATION: US/09/786,675A

TIME: 10:20:22

Input Set : A:\BB-1240 Seq List - Corrections.txt

Output Set: N:\CRF3\09192001\I786675A.raw

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:881 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17